

GenCore version 4.5									
Copyright (c) 1993 - 2000	Compugen Ltd.	P98091	bos taurus	P98467	herpes simplex	P982450	dictyocaulus	P984702	dictyocaulus
OM protein - protein search, using sw model		P98091	bovin	P982450	herpes simplex	P982450	dictyocaulus	P984702	dictyocaulus
Run on:	March 1, 2001, 16:16:37 ; Search time 91.75 Seconds	P98091	bovin	P982450	dictyocaulus	P984702	dictyocaulus	P984702	dictyocaulus
Title:	US-09-331-631A-3_COPY_29_73	51.5	20.4	52.5	1	Y107_MEJJA			
Sequence:	1 SEQDQVEECKRQCMLET.....RCVSDQDKFEEEDIDNSKYD 45	51.5	20.4	56.3	1	MUC5_BOVIN			
Scoring table:	BLOSUM62	51.5	20.4	86.0	1	UL52_HSV6U			
Searched:	Gapop 10.0 , Gapext 0.5	51.5	20.4	86.0	1	UL52_HSV6Z			
total number of hits satisfying chosen parameters:	88757	51.5	20.4	1557	1	DVAL_DCIV			
Minimum DB seq length: 0		51.5	20.4	418	1	CD15_HUMAN			
Maximum DB seq length: 200000000		51.5	20.4	418	1	FTHA_CHICK			
Post-processing: Minimum Match 0%		51.5	20.4	418	1	AR82_YESTERDAY			
Maximum Match 100%		51.5	20.4	893	1	YMG2_CAEEL			
Listing first 45 summaries		51.5	20.4	1231	1	CFAH_HUMAN			
database : SwissProt_39;*		51.5	20.4	1370	1	CD15_HUMAN			
Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		51.5	20.4	2261_HUMAN		Q14202_homo_sapien			
RESULTS		51.5	20.4	264	1	RPOD_METH			
88757		51.5	20.4	50.5	50.5	026144_methanobacter			
SUMMARIES		51.5	20.4	50.5	50.5	026144_methanobacter			
ALIGNMENTS		51.5	20.4	50.5	50.5	026144_methanobacter			
RESULT 1		51.5	20.4	50.5	50.5	026144_methanobacter			
VCLB_GOSHI		51.5	20.4	50.5	50.5	026144_methanobacter			
ID VCLB_GOSHI		51.5	20.4	50.5	50.5	026144_methanobacter			
STANDARD; PRT; 588 AA.		51.5	20.4	50.5	50.5	026144_methanobacter			
AC P09801;		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 01-MAR-1989 (Rel. 10, Created)		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 01-MAR-1989 (Rel. 10, Last sequence update)		51.5	20.4	50.5	50.5	026144_methanobacter			
DE VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).		51.5	20.4	50.5	50.5	026144_methanobacter			
OS Gossypium hirsutum (Upland cotton).		51.5	20.4	50.5	50.5	026144_methanobacter			
OT Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.		51.5	20.4	50.5	50.5	026144_methanobacter			
RN [1]		51.5	20.4	50.5	50.5	026144_methanobacter			
RP		51.5	20.4	50.5	50.5	026144_methanobacter			
RA Chilan C.A., Pyle J.B., Legocki A.B., Dure L. III;		51.5	20.4	50.5	50.5	026144_methanobacter			
RT Developmental biochemistry of cotyledon seed embryogenesis and germination. XVII. DNA and amino acid sequences of the members of the Storage protein families.;		51.5	20.4	50.5	50.5	026144_methanobacter			
RT Plant Mol. Biol. 7:475-489(1996).		51.5	20.4	50.5	50.5	026144_methanobacter			
RL		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
-! FUNCTION: SEED STORAGE PROTEIN.		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
BODIES		51.5	20.4	50.5	50.5	026144_methanobacter			
-! SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONGYCININ, ETC.).		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
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CC		51.5	20.4	50.5	50.5	026144_methanobacter			
-! SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
CONVICILIN		51.5	20.4	50.5	50.5	026144_methanobacter			
CONGYCININ		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 01-MAR-1989 (Rel. 10, Last sequence update)		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 15-JUL-1999 (Rel. 38, Last annotation update)		51.5	20.4	50.5	50.5	026144_methanobacter			
DE VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).		51.5	20.4	50.5	50.5	026144_methanobacter			
OS Gossypium hirsutum (Upland cotton).		51.5	20.4	50.5	50.5	026144_methanobacter			
OT Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.		51.5	20.4	50.5	50.5	026144_methanobacter			
RN [1]		51.5	20.4	50.5	50.5	026144_methanobacter			
RP		51.5	20.4	50.5	50.5	026144_methanobacter			
RA Chilan C.A., Pyle J.B., Legocki A.B., Dure L. III;		51.5	20.4	50.5	50.5	026144_methanobacter			
RT Developmental biochemistry of cotyledon seed embryogenesis and germination. XVII. DNA and amino acid sequences of the members of the Storage protein families.;		51.5	20.4	50.5	50.5	026144_methanobacter			
RT Plant Mol. Biol. 7:475-489(1996).		51.5	20.4	50.5	50.5	026144_methanobacter			
RL		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
-! FUNCTION: SEED STORAGE PROTEIN.		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
BODIES		51.5	20.4	50.5	50.5	026144_methanobacter			
-! SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGYCININ, ETC.).		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
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CC		51.5	20.4	50.5	50.5	026144_methanobacter			
CONVICILIN		51.5	20.4	50.5	50.5	026144_methanobacter			
CONGYCININ		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 01-MAR-1989 (Rel. 10, Last sequence update)		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 15-JUL-1999 (Rel. 38, Last annotation update)		51.5	20.4	50.5	50.5	026144_methanobacter			
DE VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).		51.5	20.4	50.5	50.5	026144_methanobacter			
OS Gossypium hirsutum (Upland cotton).		51.5	20.4	50.5	50.5	026144_methanobacter			
OT Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.		51.5	20.4	50.5	50.5	026144_methanobacter			
RN [1]		51.5	20.4	50.5	50.5	026144_methanobacter			
RP		51.5	20.4	50.5	50.5	026144_methanobacter			
RA Chilan C.A., Pyle J.B., Legocki A.B., Dure L. III;		51.5	20.4	50.5	50.5	026144_methanobacter			
RT Developmental biochemistry of cotyledon seed embryogenesis and germination. XVII. DNA and amino acid sequences of the members of the Storage protein families.;		51.5	20.4	50.5	50.5	026144_methanobacter			
RT Plant Mol. Biol. 7:475-489(1996).		51.5	20.4	50.5	50.5	026144_methanobacter			
RL		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
-! FUNCTION: SEED STORAGE PROTEIN.		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
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CC		51.5	20.4	50.5	50.5	026144_methanobacter			
CONVICILIN		51.5	20.4	50.5	50.5	026144_methanobacter			
CONGYCININ		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 01-MAR-1989 (Rel. 10, Last sequence update)		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 15-JUL-1999 (Rel. 38, Last annotation update)		51.5	20.4	50.5	50.5	026144_methanobacter			
DE VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).		51.5	20.4	50.5	50.5	026144_methanobacter			
OS Gossypium hirsutum (Upland cotton).		51.5	20.4	50.5	50.5	026144_methanobacter			
OT Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.		51.5	20.4	50.5	50.5	026144_methanobacter			
RN [1]		51.5	20.4	50.5	50.5	026144_methanobacter			
RP		51.5	20.4	50.5	50.5	026144_methanobacter			
RA Chilan C.A., Pyle J.B., Legocki A.B., Dure L. III;		51.5	20.4	50.5	50.5	026144_methanobacter			
RT Developmental biochemistry of cotyledon seed embryogenesis and germination. XVII. DNA and amino acid sequences of the members of the Storage protein families.;		51.5	20.4	50.5	50.5	026144_methanobacter			
RT Plant Mol. Biol. 7:475-489(1996).		51.5	20.4	50.5	50.5	026144_methanobacter			
RL		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
-! FUNCTION: SEED STORAGE PROTEIN.		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
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CC		51.5	20.4	50.5	50.5	026144_methanobacter			
CONVICILIN		51.5	20.4	50.5	50.5	026144_methanobacter			
CONGYCININ		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 01-MAR-1989 (Rel. 10, Last sequence update)		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 15-JUL-1999 (Rel. 38, Last annotation update)		51.5	20.4	50.5	50.5	026144_methanobacter			
DE VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).		51.5	20.4	50.5	50.5	026144_methanobacter			
OS Gossypium hirsutum (Upland cotton).		51.5	20.4	50.5	50.5	026144_methanobacter			
OT Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.		51.5	20.4	50.5	50.5	026144_methanobacter			
RN [1]		51.5	20.4	50.5	50.5	026144_methanobacter			
RP		51.5	20.4	50.5	50.5	026144_methanobacter			
RA Chilan C.A., Pyle J.B., Legocki A.B., Dure L. III;		51.5	20.4	50.5	50.5	026144_methanobacter			
RT Developmental biochemistry of cotyledon seed embryogenesis and germination. XVII. DNA and amino acid sequences of the members of the Storage protein families.;		51.5	20.4	50.5	50.5	026144_methanobacter			
RT Plant Mol. Biol. 7:475-489(1996).		51.5	20.4	50.5	50.5	026144_methanobacter			
RL		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
-! FUNCTION: SEED STORAGE PROTEIN.		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
CC		51.5	20.4	50.5	50.5	026144_methanobacter			
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CC		51.5	20.4	50.5	50.5	026144_methanobacter			
CONVICILIN		51.5	20.4	50.5	50.5	026144_methanobacter			
CONGYCININ		51.5	20.4	50.5	50.5	026144_methanobacter			
DT 01-MAR-1989 (Rel. 10, Last sequence update)		51.5</							

AC P09799;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE VICTILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).  
OS Gossypium hirsutum (Upland cotton).  
OC Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta;  
OC Malvales; Malvaceae; Gossypium.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chian C.A., Borroto K., Kamalay J.A., Dure L. III;  
RT "Developmental biochemistry of cottonseed embryogenesis and alpha  
germination. XIX. Sequences and genomic organization of the alpha  
globulin (vicilin) genes of cottonseed.";  
RL Plant Mol. Biol. 9:533-546(1987).  
CC !- FUNCTION: SEED STORAGE PROTEIN.  
CC !- SUBCELLULAR LOCATION: COMPLENDARY MEMBRANE-BOUNDED VACUOLAR PROTEIN  
BODIES.  
CC !- SIMILARITY: TO OTHER 75 SEED STORAGE PROTEINS (PHASEOLIN, VICILIN,  
CONVICILIN, CONGLICININ, ETC.).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
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or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; M13378; AAA31069.1; --.  
DR PIR; S06398; P06398;  
DR IPI; 5547; 1CAK.  
DR INTERPRO; IPR001113; --.  
DR PFAM; PF00546; Seedsstore\_7s; 1.  
KW Seed storage protein; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 605 AA; 71049 MW; C9DB9371C976953B CRC64;  
SQ -----  
Query Match 28.6%; Score 72; DB 1; length 605;  
Best Local Similarity 42.5%; Pred. No. 0.26;  
Matches 17; Conservative 9; Mismatches 10; Indels 4; Gaps 3;  
QY 1 SEFD-RQEVEBECKRQCMQLETSGMRRCVSCQCDKRFEEEDI 39  
Db 33 SEDPQQQRVEDCRKRC-QLETRGTEQ - DKCENSSETORL 69  
RESULT 3  
AGR\_LUFCA STANDARD: PRT; 47 AA.  
ID AGR\_LUFCA STANDARD: PRT; 47 AA.  
AC P56568;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DE 6.5-K ARGinine/Glutamate-Rich Polypeptide (6.5K-AGRP).  
OS Luffa cylindrica (Smooth loofah) (Sponge gourd).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicots; Malvales; Malvaceae; Luffa.  
OC Cucurbitales; Cucurbitaceae; Luffa.  
RN [1]  
RP SEQUENCE.  
RC TISSUE=SEED;  
RX MEDLINE=97357433; PubMed=9214759;  
RA Kimura M., Park S.S., Sakai R., Yamashiki N., Funatsu G.;  
RT "Primary structure of 6.5-k-arginine/glutamate-rich polypeptide from  
the seeds of sponge gourd (*Luffa cylindrica*).";  
RL Biosci. Biotechnol. Biochem. 61:984-988(1997).  
CC !- FUNCTION: STORAGE PROTEIN WHICH PROVIDES NITROGEN AND CARBON  
CC RESERVES DURING GERMINATION AND SEEDLING GROWTH.  
CC !- MASS SPECTROMETRY: MW=593.39; METHOD=MALDI.

RESULT 4  
TSPL\_HUMAN STANDARD: PRT; 1170 AA.  
ID TSPL\_HUMAN STANDARD: PRT; 1170 AA.  
AC P07596;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-AUG-1988 (Rel. 08, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE THROMBOSPDIN 1 PRECURSOR.  
GN THBS1 OR TSPI OR TSP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ENDOTHELIAL CELLS;  
RN MEDLINE=875617; PubMed=2430973;  
RX Lawler J., Hynes R.O.;  
RT "The structure of human thrombospondin, an adhesive glycoprotein with  
multiple calcium-binding sites and homologies with several different  
proteins";  
RL J. Cell Biol. 103:1635-1648(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88139590; PubMed=2918029;  
RX Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L.,  
RA Baumgartel D.M., Rotwein P., Frazier W.A.;  
RT "Complete thrombospondin mRNA sequence includes potential regulatory  
sites in the 3' untranslated region";  
RL J. Cell Biol. 108:729-736(1989).  
RN [3]  
RP SEQUENCE OF 1-397 FROM N.A.  
RX MEDLINE=87157592; PubMed=3030396;  
RA Kobayashi S., Eden-McCutchan F., Framson P., Bernstein P.;  
RT "Partial amino acid sequence of human thrombospondin as determined by  
analysis of cDNA clones: homology to malarial circumsporozoite  
proteins";  
RL Biochemistry 25:8418-8425(1986).  
RN [4]  
RP SEQUENCE OF 1-374 FROM N.A.  
RX MEDLINE=86287276; PubMed=3461443;  
RA Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;  
RT "Characterization of a cDNA encoding the heparin and collagen binding  
domains of human thrombospondin";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).  
RN [5]  
RP SEQUENCE OF 1-166 FROM N.A.  
RX MEDLINE=89291870; PubMed=2545457;  
RA LaFerriere C.D., German T.M., Dixit V.M.;  
RT "Characterization of the promoter region of the human thrombospondin  
gene DNA sequences within the first intron increase transcription";  
RL J. Biol. Chem. 264:11222-11227(1989).  
RN [6]  
RP SEQUENCE OF 1028-1170 FROM N.A.  
RA La Fleur M., Jobin C., Gauthier J., Kretzschmar C.G.;  
RL Submitted (XXI-1992) to the EMBL/GenBank/DDBJ databases.  
CC !- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND  
CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,

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RESULT	5	Query Match	26.6%	Score	67;	DB	1;	Length	1170;
TPSP1_MOUSE	ID	TPSP1_MOUSE	STANDARD;	PRT;	1170 AA.				
AC	P35441;								
DT	01-JUN-1994	(Rel.	29,	Created)					
DT	01-JUN-1994	(Rel.	29,	Last sequence update)					
DE	01-OCT-1995	(Rel.	34,	Last annotation update)					
GN	THBS1 OR TPSP1.								
OS	Mus musculus (Mouse)								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	Medline=92147841; Pubmed=1774063;								
RA	Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J., Jenkins N.A.;								
RT	"Characterization of the murine thrombospondin gene.";								
RL	Genomics 11:587-600(1991).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RX	Medline=92147683; Pubmed=1371115;								
RA	Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F., Dixit V.M.;								
RT	"Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development";								
RL	J. Biol. Chem. 267:3274-3281(1992).								
RN	[3]								
RP	SEQUENCE OF 1-490 FROM N.A.								
RX	Medline=9037556; Pubmed=22398070;								
RA	Bornstein P., Alföldi D., Devarayalu S., Framson P., Li P., "Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";								
RT	J. Biol. Chem. 265:16691-16698(1990).								
RL	J. Biol. Chem. 265:16691-16698(1990).								
CC	"- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN, LAMININ AND TYPE V COLLAGEN."								
CC	"- SUBUNIT: HOMOTIMER, CROSS-LINKED BY DISULFIDE BONDS."								
CC	"- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY."								
CC	"- SIMILARITY: CONTAINS 1 VWF DOMAIN."								
CC	"- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS."								
CC	"- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-3 TSP REPEATS (WHICH BIND CALCIUM)."								
CC	"- SUBUNIT: HOMOTIMER, CROSS-LINKED BY DISULFIDE BONDS."								
CC	"- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY."								
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CC	"- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-3 TSP REPEATS (WHICH BIND CALCIUM)."								
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CC	"- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS."								
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CC	"- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS."								
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CC	"- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY."								
CC	"- SIMILARITY: CONTAINS 1 VWF DOMAIN."			</					



CC	RATE OF SUCROSE UPTAKE IN THE COTYLEDON.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	DRINTERPRO; ITR001113; -.
CC	DRPFAM; PF00516; Seeds, store_7s; 1.
CC	DRTRANSPORT; Sugar transport; Signal; Membrane.
FT	SIGNAL 1
FT	CHAIN 30 524 AA; 60522 MW; 0251E59076EF341 CREG4;
FT	SEQUENCE 524 AA; 60522 MW; 0251E59076EF341 CREG4;
FT	ATIL_VACCV
ID	ATIL_VACCV
AC	P24759;
DT	01-MAR-1992 (Rel. 21, 'Created')
Qy	2 ENDQEQEECKHQCMQLE--ISGQMRCVSYQCDK 33
Db	34 EEDDPPLVTCKHOCOOQQYEGDKRYCQLQSCDR 67
RESULT 7	8
Query Match	25.8%; Score 65; DB 1; Length 1173;
Best Local Similarity	39.5%; Pred. No. 3.2;
Matches	15; Conservative 5; Mismatches 12; Indels 6; Gaps 2;
Qy	13 ROCMQL-E---TSGQMRCC-VSQCDKREEDIWRY 44
Db	407 RSCDSLNNPCGSSVQTRSCOIQDCDKRKGQDGGWSIW 444
SEQUENCE	1173 AA; 130019 MW; A9F036D6516C0F24 GRC64;
SBP_SOBN	STANDARD; PRT; 524 AA.
AC	Q04672;
DT	01-JUN-1994 (Rel. 29, 'Created')
DT	01-JUN-1994 (Rel. 29, 'Last sequence update')
DE	SUCROSE-BINDING PROTEIN PRECURSOR (SBP).
GN	SBP.
OS	Glycine max (Soybean).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; eudicots; Rosidae; eurosids I;
OC	Fabales; Fabaceae; Papilionoideae; Glycine.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	Medline=91310644; PubMed=1856205;
RA	Amegadzie B.Y., Ahn B.-Y., Moss B.;
RT	"Identification, sequence, and expression of the gene encoding a Mr 35,000 subunit of the vaccinia virus DNA-dependent RNA polymerase.";
RL	J. Biol. Chem. 266:13712-13718(1991).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	Medline=92124754; PubMed=173311;
RA	Amegadzie B.Y., Sisler J.R., Moss B.;
RT	"Frame-shift mutations within the vaccinia virus A-type inclusion protein gene.";
RT	Virology 196:777-782(1992).
RL	[3]
RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RX	Medline=92074241; PubMed=1962448;
RA	de Carlos A., Paez E.;
RT	"Isolation and characterization of mutants of vaccinia virus with a modified 94-kDa inclusion protein.";
RL	Virology 185: 763-778(1991).
CC	-!- FUNCTION: Mature viruses are occluded into the ATI, and it has been assumed that such bodies protect the virus during dissemination from animal to animal.
CC	-!- MISCELLANEOUS: A characteristic feature of ATI is the formation of large masses with no surrounding membranes in the cytoplasm of infected cells.
CC	-!- SIMILARITY: 92% IDENTITY TO COWPOX VIRUS A-TYPE INCLUSION PROTEIN N-TERMINAL.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

	Query Match	Score	DB	Length
	Best local Similarity	40.6%	Pred. No.	17
	Matches	13;	Conservative	11;
CC	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).			
CC	or send an email to license@isb-sib.ch).			
DR	M61187; AAA48321.1; -			
DR	M76571; AAA8275.1; -			
DR	X57318; CAA40574.1; -			
PIR	A41701; WNYZ94.			
DR	S29908; S29908.			
FT	CONFFLICT 587 588	KQ -> SK (IN REF. 3).		
FT	CONFFLICT 610 610	R -> H (IN REF. 3).		
FT	CONFFLICT 618 618	R -> RR (IN REF. 3).		
FT	CONFFLICT 682 682	S -> R (IN REF. 3).		
SQ	SEQUENCE 724 AA; 84235 MW; C560CF61C9903028 CRC64;			
RESULT 9				
ATI_CAMPIC	ATI_CAMPIC STANDARD; PRT; 726 AA.			
ID	005482; Q05482; 01-FEB-1995 (Rel. 31, Created)			
AC	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	01-FEB-1995 (Rel. 31, Last annotation update)			
DE	A-TYPE INCLUSION PROTEIN (ATI).			
OS	Campylopo virus (strain CP-1).			
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
OC	Orthopoxvirus.			
RN	[1] 550 KRRNVWELS-RLRRDIKECDK-YKEDDKAK 579			
RESULT 10				
ATI_COMPX	ATI_COMPX STANDARD; PRT; 1284 AA.			
ID	005482; Q05482; 01-AUG-1990 (Rel. 15, Created)			
AC	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	01-AUG-1990 (Rel. 15, Last annotation update)			
DE	A-TYPE INCLUSION PROTEIN (ATI).			
GN	ATI.			
OS	Cowpox virus (CPV).			
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;			
OC	Orthopoxvirus.			
RN	[1] SEQUENCE FROM N.A.			
RP	SEQUENCE OF 1-109 FROM N.A.			
RX	MEDLINE=88089536; PubMed=2826668;			
RA	"Cloning and characterization of the gene encoding the major protein			
RT	of the A-type inclusion body of cowpox virus.";			
RL	J. Gen. Virol. 69:35-47(1988).			
RN	[2] MEDIEN=CPR06;			
RP	SEQUENCE OF 88111568; PubMed=2828037;			
RX	MEDLINE=88111568; PubMed=2828037;			
RA	Patel D.D., Pickup D.J.,			
RT	"Messenger RNAs of a strongly-reexpressed late gene of cowpox virus			
RT	contain 5'-terminal poly(A) sequences.";			
RL	EMBO J. 6:3787-3794(1987).			
EMBO J. 6:3787-3794(1987).	-!- FUNCTION: MATURE VIRUSES ARE OCCLUDED INTO THE ATI, AND IT HAS			
CC	BEN ASSUMED THAT SUCH BODIES PROTECT THE VIRUS DURING			
CC	DISSEMINATION FROM ANIMAL TO ANIMAL.			
CC	-!- MISCELLANEOUS: A CHARACTERISTIC FEATURE OF ATI IS THE FORMATION OF			
CC	LARGE MASSES WITH NO SURROUNDING MEMBRANES IN THE CYTOPLASM OF			
CC	INFECTED CELLS.			
CC	.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).			
CC	.			
DR	EMBL; D00319; BRA0022.1; -			
DR	EMBL; X06343; CAA29850.1; -			
DR	PIR; JQ0006; WNYZAI.			
KW	Late protein; Repeat.			
FT	DOMAIN 611 912	10 x APPROXIMATE TANDEM REPEATS.		
FT	REPEAT 611 637	1.		
FT	REPEAT 638 665	2.		
FT	REPEAT 666 689	3.		
FT	REPEAT 690 720	4.		
FT	REPEAT 721 751	5.		
FT	REPEAT 752 780	6.		
FT	REPEAT 781 811	7.		
FT	REPEAT 812 842	8.		
FT	REPEAT 843 871	9.		
FT	REPEAT 872 912	10.		
FT	SEQUENCE 1284 AA; 150329 MW; F7904C9E1DE8D012 CRC64;			
Query Match	22.6%; Score 57; DB 1; Length 1284;			
Best Local Similarity	40.6%; Pred. No. 29;			
Matches	13; Conservative 11; Mismatches 6; Indels 2; Gaps 2;			

RESULT	11	12 KRCMQLETSQMRRCVSVQDQKRFEDIWNSK 43
ID	PPP6_RAT	STANDARD; PRT; 305 AA.
ID	PPP6_RAT	STANDARD; PRT; 305 AA.
AC	064620;	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)	01-AUG-1988 (Rel. 08, Last sequence update)
DT	15-JUL-1998 (Rel. 36, Last annotation update)	15-DEC-1998 (Rel. 37, Last annotation update)
DE	SERINE/THYREONINE PROTEIN PHOSPHATASE 6 (EC 3.1.3.16) (PPP6) (PROTEIN PHOSPHATASE VI) (PPV).	ENDOPLASMIN PRECURSOR (HEAT SHOCK 108 KDA PROTEIN) (HSP108)
DE	PPP6C OR PPV.	(HSP 108) (TRANSTERRIN-BINDING PROTEIN).
GN	Rattus norvegicus (Rat). Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. [1]	TIRAI.
RP	SEQUENCE FROM N.A.	OS Galillus galilus (chicken).
RC	STRAIN=SPAGUE-DAWLEY; TISSUE=TESTIS, AND BRAIN;	OC Euksyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
RC	PPMLINE=04357839; PubMed=8077208;	OC Galillus.
RA	Becker W., Kenrrup H., Klumpp S., Schultz J.E., Joost H.G.;	[1]
RT	"Molecular cloning of a protein serine/threonine phosphatase containing a putative regulatory tetratricopeptide repeat domain.";	RP SEQUENCE FROM N.A.
RT	J. Biol. Chem. 269:22586-22592(1994).	RX MEDLINE=87076542; PubMed=3024703;
RL	- - FUNCTION: MAY FUNCTION IN CELL CYCLE REGULATION.	RA Kilomaa M.S., Weigel N.L., Kleinhenz D.A., Beattie W.G., Connally O.M., March C., Zarucki-Schulz T., Schrader W.T., O'Malley B.W.
CC	- - CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H2O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THYREONINE SPECIFIC).	RT "Amino acid sequence of a chicken heat shock protein derived from the complementary DNA nucleotide sequence.";
CC	- - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).	RT Biochemistry 25:6244-6251(1986).
CC	- - TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SPLEEN, BRAIN AND LUNG.	RN [2]
CC	- - SIMILARITY: BELONGS TO THE PPP FAMILY OF PHOSPHATASES. PP-V SUBFAMILY.	RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
CC	-----	RX MEDLINE=94220155; PubMed=8166742;
CC	-----	RA Hayes G.R., Himpler B.S., Weiner K.X.B., Lucas J.J.; RT "A chicken transferrin binding protein is heat shock protein 108.";
CC	-----	RT Kleinsek D.A., Beattie W.G., Tsai M.J., O'Malley B.W.; RT Molecular cloning of a steroid-regulated 108k heat shock protein gene from hen ovary.";
CC	-----	RT Nucleic Acids Res. 14:10053-10069(1986).
CC	-----	RN [4]
CC	-----	RP TISSUE=OVIDUCT;
CC	-----	RA Porsgren M.;
CC	-----	RL Submitted (XXX-1987) to the EMBL/GenBank/DDBJ databases.
CC	-----	CC - - SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC	-----	CC - - SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
CC	-----	CC - - SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
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DR	PROSITE; PS00125; SBR_TIR_PHOSPHATASE; 1.	CC DR EMBL; M14772; AAA4826.1; -.
DR	KW Hydrolase; Iron; Manganese.	DR EMBL; M31321; AAA48827.1; -.
FT	METAL_ 53 53 IRON (BY SIMILARITY).	DR EMBL; X04951; CAA28629.1; -.
FT	METAL_ 55 55 IRON (BY SIMILARITY).	DR PIR; A24461; HHG10.
FT	METAL_ 81 81 IRON AND MANGANESE (BY SIMILARITY).	DR PIR; JC2205; JC2205.
FT	METAL_ 113 113 MANGANESE (BY SIMILARITY).	DR HSSP; P02839; IAMB.
FT	ACYL_SITE 114 114 GENERAL ACID (BY SIMILARITY).	DR INTERPRO; IPR000886; -.
FT	METAL_ 163 163 MANGANESE (BY SIMILARITY).	DR INTERPRO; IPR001404; -.
FT	METAL_ 237 237 MANGANESE (BY SIMILARITY).	DR PFAM; PF00183; HSP90; 1.
SO	SEQUENCE 305 AA; 351.06 MW; A91FF993FBDBF110 CRC64;	DR PRINTS; PRO0075; HEATSHOCK90.
DR	PROSITE; PS00014; ER_TARGET; 1.	DR PROSITE; PS00298; HSP90; 1.
DR	PROSITE; PS00298; HSP90; 1.	KW Chaperone; Endoplasmic reticulum; Glycoprotein; Calcium-binding; Signal; Heat shock.
FT	SIGNAL 1 21 POTENTIAL.	FT SIGNAL 1 21 POTENTIAL.
FT	CHAIN 61 61 ENDOPLASMIN.	FT CARBOHYD 61 795 N-LINKED (GLCNAC, . . .) (POTENTIAL).
FT	CARBOHYD 61 795 N-LINKED (GLCNAC, . . .) (POTENTIAL).	FT CARBOHYD 106 106 N-LINKED (GLCNAC, . . .) (POTENTIAL).
FT	CARBOHYD 216 216 N-LINKED (GLCNAC, . . .) (POTENTIAL).	FT CARBOHYD 444 444 N-LINKED (GLCNAC, . . .) (POTENTIAL).
FT	CARBOHYD 480 480 N-LINKED (GLCNAC, . . .) (POTENTIAL).	FT CARBOHYD 501 501 N-LINKED (GLCNAC, . . .) (POTENTIAL).
FT	CARBOHYD 792 795 PREVENT SECRETION FROM ER.	



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DR EMBL; X87581; CAA60885.1;  
DR ZFIN; ZDB-GENE-980526-176; CYCD1.  
DR INTERPRO; IPR000553;  
DR PFAM; PF0134; cyclin; 1.  
DR PROSITE; PS00292; CYCLINS; 1.  
KW cyclin; cell cycle; Cell division.  
SQ SEQUENCE 291 AA: FA5274CBB46D5EF CRC64;

Query Match 21.4%; Score 54; DB 1; Length 291;  
Best local similarity 38.5%; Pred. No. 16;  
Matches 15; Conservative 7; Mismatches 11; Indels 6; Gaps 2;

Qy 10 ECKRQEMQ----LENS-GQMRRCVSQCDKRFEDIDWS 42  
Db 242 DCLRSQEQTESLLESSLRQAQHISTETKVEEDVDSL 280

Search completed: March 1, 2001, 16:16:38  
Job time: 418 sec

